

Nickolai N. Alexandrov
~~~~~

Ceres Inc.

3007 Malibu Canyon Rd  
Malibu, CA 90265

Email: nicka@ncicrf.gov, nicka@amgen.com

Phone: (310) 317-8903

Fax: (310) 317-8998

WWW: <http://www-lmmb.ncicrf.gov/~nicka/info.html>



July, 1999

Education:

~~~~~

1978/1984 Moscow Engineering-Physics Institute, Moscow, Russia

Main subjects: Functional Analysis, Analytical Geometry, Linear Algebra, Equations of Mathematical Physics, Theory of Functions of a Complex Variable, Differential Equations, Mathematical Statistics, Programming, General Physics, Field Theory, Theoretical Physics, Quantum Mechanics, Statistical Physics, Nuclear Physics, General Chemistry, Physical Chemistry, Organic Chemistry, General Biology, Molecular Biology, Physical Chemistry of Biopolymers.

1985/1989 - Research Institute for Genetics of microorganisms, Moscow, Russia.

Main subject: Molecular biology.

Academic degrees:

~~~~~

1984 B.S., M.S., Physics, Moscow Engineering-Physics Institute, Moscow, Russia

1989 Ph.D., Molecular Biology, Institute for Genetics of Microorganisms, Moscow, Russia.

Professional Experience:

~~~~~

1998-present: Manager for Bioinformatics, Ceres Inc., Malibu, CA, USA.

1996-1998: Computational Scientist, Amgen Inc., Thousand Oaks, CA, USA.

1993-1996: Visiting Fellow in the Laboratory of Mathematical Biology headed by Dr. J.Maizel, NCI-NIH, Frederick, MD, USA.

1993 (Jan-Oct): Postdoctoral Fellow at the Protein Engineering Research Institute, Department of Dr. H.Nakamura, Suita, Japan

1990-1992: ASPS Postdoctoral Fellow in the laboratory of Prof. NG, Chemistry Department, Faculty of Science, Kyoto University, Kyoto, Japan.

1984-1989: Research Assistant, Junior Scientist. Institute of Genetics and Selection of Industrial Microorganisms, Moscow, Russia.

Professional Activities:

~~~~~

Programming:

-----

Computers: DEC, SUN, SGI, Titan 3000, supercomputers Hitachi, Fujitsu, Cray.

Operation systems: UNIX, OS, VMS.

Programming languages: C, Fortran.

Program products: program packages for DNA/protein sequence analysis DNA-SUN; software for museum of microorganisms; program SARF for protein structure comparison; program 123D for fold recognition (SARF2 and 123D are available via WWW: <http://www-lmmb.ncifcrf.gov/~nicka/info.html>).

Teaching experience:

-----

Informatics and computer applications in molecular biology.  
Course for postgraduate students. Moscow Institute for genetics of microorganisms. 1989-1990.

Awards:

-----

Honors Graduate, Moscow Engineering-Physics Institute,  
Moscow, Russia, 1984

JSPS fellowship, Japan Society of the Promotion of Science,  
Tokyo, Japan, 1990

Programming of thinking games, golden medals on the 1st and 2nd World  
Computer Olympiad, London, 1990, 1991.

Refereeing Service:

-----

Journal of Molecular Biology, CABIOS, Protein Engineering, BioSystems:  
Computer Genetics, Pacific Biocomputing Symposium, Biochimica et Biophysica Acta.

Invited Talks:

-----

Iterative strategy for searching distant homologs in databases.  
UCLA, Los Angeles, CA, April 1997

Blind predictions of protein structures with 123D.

Critical Assessment of Structure Prediction (CAPS-2),  
Asilomar, CA, December 1996.

Fold recognition with contact capacity potentials and secondary  
structure prediction: program 123D. National Institute for Genetics,  
Mishima, Japan, December 1996.

Effect of secondary structure prediction on fold recognition.  
Genome Informatics 1996, Tokyo, Japan, December 1996

Algorithms for Protein Structure Comparison.  
USC, Los Angeles, CA, March 1996

Nontopological threading.  
UCLA, Los Angeles, CA, May 1995

Biological meaning and statistical significance of the common spatial  
arrangements of backbone fragments in protein structures.  
Protein Engineering Research Institute (PERI),  
Suita, Japan, September 1992

SARF: a program for comparison of protein structures.  
European Molecular Biology Laboratory (EMBL),  
Heidelberg, Germany, August 1991.

#### Publications

-----  
Bolotin A.P., Sorokin A.V., Alexandrov N.N., Danilenko V.N., Kozlov  
Yu.I. DNA sequence of actinomyces plasmid pSB 24.2. Dokl. Acad. of Sci. USSR,  
v.283, N 4, pp.1014-1017., 1985.

Bolotin A.P., Sorokin A.V., Alexandrov N.N., Danilenko V.N., Kozlov  
Yu.I. Study of Streptomyces replication: DNA sequence of plasmid pSB 24.2.  
Antibiotics and medical biotechnology, 1985, v.30, N 11, pp. 804-811.

Alexandrov N.N., Mironov A.A. Recognition of Escherichia coli promoters  
in DNA sequence. Molekulyarnaya Biologia (USSR), 1987, v.20, pp.242-249.

Mironov A.A., Alexandrov N.N., Lunovskaya-Gurova L.V., Kister A.E.  
Program package for DNA sequence analysis. Molekulyarnaya Biologia (USSR), 1987,  
21, 672-677.

Mironov A.A., Alexandrov N.N. Rapid method for homology search.  
Biophisika (USSR), 1988, v.33, pp.229-232.

Mironov A.A., Alexandrov N.N. Statistical method for rapid homology  
search. Nucleic Acids Res. 1988, v.16, p.5169-5173.

Alexandrov A.A., Alexandrov N.N., Borodovsky M.Yu., Kister A.E.,  
Kalambet Yu.A., Mironov A.A., Pevzner P.A., Shepelev V.V. Computer  
analysis of genetic texts (Ed. by Frank-Kamenetskii M.D.) Moscow, Nauka, 1989.  
(in Russian).

Alexandrov N.N. Signal Recognition in DNA sequences. Dissertation, 1989 (in Russian).

Alexandrov N.N., Mironov A.A. Application of a new method of pattern recognition in DNA sequence analysis: a study of E.coli promoters. Nucl. Acids Res., 1990, v.18, p.1847-1852.

Alexandrov N.N. Local multiple alignment by consensus matrix. CABIOS, 1992, v.8, p.339-345.

Alexandrov N., Takahashi K., Go N.. Common spatial arrangements in homologous and nonhomologous proteins. J. Mol. Biol., 1992, v.225, p.5-9.

Alexandrov N. Structural argument for N-terminal initiation of protein folding. Protein Sci., 1993, v.2, p.1989-1991.

Alexandrov N., Go N. Biological meaning, statistical significance and classification of local spatial similarities in nonhomologous proteins. Protein Sci., 1994, v. 3, p. 866-875.

Swindels M., Alexandrov N. Nucleotide binding in bab-bab topologies. Nature , Struct. Biol., 1994, v.1, p. 677-678.

Mironov A.A., Alexandrov N.N., Bogodanova N.Yu., Grigoriev A.V., Lebedev V., Pevzner P.A., Lyunovskaya L.V., Trukhan M.E. DNA-SUN: a software for nucleotide and amino acid sequence analysis. CABIOS, 1995 11, 331-335.

Alexandrov N. and Fischer D. Analysis of topological and nontopological structural similarities in the PDB: new examples with old structures. Proteins, 1996, 25, 354-365.

Alexandrov N. Sarfing the PDB. Protein Engineering, 1996, 9, 727-732.

Alexandrov N., Nussinov R., Zimmer R. Fast Protein Fold Recognition via Sequence to Structure alignment and contact capacity potentials. Pacific Symposium of Biocomputing'1996, 1995, (Hunter, L. and Klein, T.E. eds.), 53-72.

Alexandrov N.N. and Solovyev V.V. Effect of secondary structure prediction on protein fold recognition and database search. The seventh workshop on genome informatics (GIW'96), Tokyo, 1996, 119-127.

Alexandrov NN. and Luethy R. Alignment algorithm for homology modeling and threading. submitted, 1997.

Alexandrov N.N. and Solovyev V.V. Statistical significance of ungapped alignments. to be published PBS'98. 1998.

Alexandrov NN, Solovyev VV, and Zimmer R. Protein fold recognition beyond sequence similarity. in preparation, 1997.